



RAW SEQUENCE LISTING **ERROR REPORT**

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Application Serial Number: 09/424,347
Source: OPE
Date Processed by STIC: 4/30/02

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TECH CENTER 1600/2900

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

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<http://www.uspto.gov/web/offices/pac/checker>

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Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
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Revised 01/29/2002



OIPE

Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/424,347

DATE: 04/30/2002
TIME: 14:45:49

Input Set : A:\49429seq.txt
Output Set: N:\CRF3\04302002\I424347.raw

RECEIVED

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TECH CENTER 1600/2900

4 <110> APPLICANT: ENDOU, Hitoshi
5 KANAI, Yoshikatsu
6 SEKINE, Takashi
7 HOSOYAMADA, Makoto
9 <120> TITLE OF INVENTION: ORGANIC ANION TRANSPORTER AND GENE
10 CODING FOR THE SAME
12 <130> FILE REFERENCE: 49429 (71526)
14 <140> CURRENT APPLICATION NUMBER: 09/424,347
C--> 15 <141> CURRENT FILING DATE: 2002-04-16
17 <150> PRIOR APPLICATION NUMBER: PCT/JP98/02171
18 <151> PRIOR FILING DATE: 1998-05-18
20 <160> NUMBER OF SEQ ID NOS: 4
22 <170> SOFTWARE: FastSEQ for Windows Version 3.0

ERRORED SEQUENCES

266 <210> SEQ ID NO: 3
267 <211> LENGTH: 0 - input 0, found 2171!
268 <212> TYPE: DNA
269 <213> ORGANISM: Human
271 <220> FEATURE:
272 <221> NAME/KEY: CDS
W--> 273 <222> LOCATION: (268)...(1956)
275 <400> SEQUENCE: 3
276 gaaagctgag ctgccctgac ccccaaagtg aggagaagct gcaagggaaa agggagggac 60
277 agatcagggg gaccggggaa gaaggaggag cagccaagga ggctgctgtc cccccacaga 120
278 gcagctcgga ctgagctccc ggagcaaccc agctgcggag gcaacggcag tgctgctcct 180
279 ccagcgaagg acagcaggca ggcagacaga cagaggtcct gggactggaa ggctcagcc 240
280 cccagccact gggctgggccc tggcccca atg gcc ttt aat gac ctc ctg cag cag 294
281 Met Ala Phe Asn Asp Leu Leu Gln Gln
282 1 5
284 gtg ggg ggt gtc ggc cgc ttc cag cag atc cag gtc acc ctg gtg gtc 342
285 Val Gly Gly Val Gly Arg Phe Gln Gln Ile Gln Val Thr Leu Val Val 25
286 10 15 20
288 ctc ccc ctg ctc ctg atg gct tct cac aac acc ctg cag aac ttc act 390
289 Leu Pro Leu Leu Met Ala Ser His Asn Thr Leu Gln Asn Phe Thr 40
290 30 35
292 gct gcc atc cct acc cac cac tgc cgc ccg cct gcc gat gcc aac ctc 438
293 Ala Ala Ile Pro Thr His His Cys Arg Pro Pro Ala Asp Ala Asn Leu 55
294 45 50
296 agc aag aac ggg ggg ctg gag gtc tgg ctg ccc cgg gac agg cag ggg 486
297 Ser Lys Asn Gly Gly Leu Glu Val Trp Leu Pro Arg Asp Arg Gln Gly

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298	60	65	70	534
300	cag cct gag tcc tgc ctc cgc ttc acc tcc ccg cag tgg gga ctg ccc			
301	Gln Pro Glu Ser Cys Leu Arg Phe Thr Ser Pro Gln Trp Gly Leu Pro			
302	75	80	85	582
304	ttt ctc aat ggc aca gaa gcc aat ggc aca ggg gcc aca gag ccc tgc			
305	Phe Leu Asn Gly Thr Glu Ala Asn Gly Thr Gly Ala Thr Glu Pro Cys			
306	90	95	100	630
308	acc gat ggc tgg atc tat gac aac agc acc ttc cca tct acc atc gtg			
309	Thr Asp Gly Trp Ile Tyr Asp Asn Ser Thr Phe Pro Ser Thr Ile Val			
310	110	115	120	678
312	act gag tgg gac ctt gtg tgc tct cac agg gcc cta cgc cag ctg gcc			
313	Thr Glu Trp Asp Leu Val Cys Ser His Arg Ala Leu Arg Gln Leu Ala			
314	125	130	135	726
316	cag tcc ttg tac atg gtg ggg gtg ctg ctc gga gcc atg gtg ttc ggc			
317	Gln Ser Leu Tyr Met Val Gly Val Leu Leu Gly Ala Met Val Phe Gly			
318	140	145	150	774
320	tac ctt gca gac agg cta ggc cgc cgg aag gta ctc atc ttg aac tac			
321	Tyr Leu Ala Asp Arg Leu Gly Arg Arg Lys Val Leu Ile Leu Asn Tyr			
322	155	160	165	822
324	ctg cag aca gct gtg tca ggg acc tgc gca gcc ttc gca ccc aac ttc			
325	Leu Gln Thr Ala Val Ser Gly Thr Cys Ala Ala Phe Ala Pro Asn Phe			
326	170	175	180	870
328	ccc atc tac tgc gcc ttc cgg ctc ctc tgc ggc atg gct ctg gct ggc			
329	Pro Ile Tyr Cys Ala Phe Arg Leu Leu Ser Gly Met Ala Leu Ala Gly			
330	190	195	200	918
332	atc tcc ctc aac tgc atg aca ctg aat gtg gag tgg atg ccc att cac			
333	Ile Ser Leu Asn Cys Met Thr Leu Asn Val Glu Trp Met Pro Ile His			
334	205	210	215	966
336	aca cgg gcc tgc gtg ggc acc ttg att ggc tat gtc tac agc ctg ggc			
337	Thr Arg Ala Cys Val Gly Thr Leu Ile Gly Tyr Val Tyr Ser Leu Gly			
338	220	225	230	1014
340	cag ttc ctc ctg gct ggt gtg gcc tac gct gtg ccc cac tgg cgc cac			
341	Gln Phe Leu Leu Ala Gly Val Ala Tyr Ala Val Pro His Trp Arg His			
342	235	240	245	1062
344	ctg cag cta ctg gtc tct gcg cct ttt ttt gcc ttc ttc atc tac tcc			
345	Leu Gln Leu Leu Val Ser Ala Pro Phe Phe Ala Phe Phe Ile Tyr Ser			
346	250	255	260	1110
348	tgg ttc ttc att gag tgc gcc cgc tgg cac tcc tcc tcc ggg agg ctg			
349	Trp Phe Phe Ile Glu Ser Ala Arg Trp His Ser Ser Ser Gly Arg Leu			
350	270	275	280	1158
352	gac ctc acc ctg agg gcc ctg cag aga gtc gcc cgg atc aat ggg aag			
353	Asp Leu Thr Leu Arg Ala Leu Gln Arg Val Ala Arg Ile Asn Gly Lys			
354	285	290	295	1206
356	cgg gaa gaa gga gcc aaa ttg agt atg gag gta ctc cgg gcc agt ctg			
357	Arg Glu Glu Gly Ala Lys Leu Ser Met Glu Val Leu Arg Ala Ser Leu			
358	300	305	310	1254
360	cag aag gag ctg acc atg ggc aaa ggc cag gca tgc gcc atg gag ctg			
361	Gln Lys Glu Leu Thr Met Gly Lys Gly Gln Ala Ser Ala Met Glu Leu			
362	315	320	325	

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364 ctg cgc tgc ccc acc ctc cgc cac ctc ttc ctc tgc ctc tcc atg ctg 1302
365 Leu Arg Cys Pro Thr Leu Arg His Leu Phe Leu Cys Leu Ser Met Leu 345
366 330 335 340
368 tgg ttt gcc act agc ttt gca tac tat ggg ctg gtc atg gac ctg cag 1350
369 Trp Phe Ala Thr Ser Phe Ala Tyr Tyr Gly Leu Val Met Asp Leu Gln 360
370 350 355 360
372 ggc ttt gga gtc agc atc tac cta atc cag gtg atc ttt ggt gct gtg 1398
373 Gly Phe Gly Val Ser Ile Tyr Leu Ile Gln Val Ile Phe Gly Ala Val 375
374 365 370
376 gac ctg cct gcc aag ctt gtg ggc ttc ctt gtc atc aac tcc ctg ggt 1446
377 Asp Leu Pro Ala Lys Leu Val Gly Phe Leu Val Ile Asn Ser Leu Gly 390
378 380 385
380 cgc cgg cct gcc cag atg gct gca ctg ctg ctg gca ggc atc tgc atc 1494
381 Arg Arg Pro Ala Gln Met Ala Ala Leu Leu Leu Ala Gly Ile Cys Ile 405
382 395 400
384 ctg ctc aat ggg gtg ata ccc cag gac cag tcc att gtc cga acc tct 1542
385 Leu Leu Asn Gly Val Ile Pro Gln Asp Gln Ser Ile Val Arg Thr Ser 425
386 410 415 420
388 ctt gct gtg ctg ggg aag ggt tgt ctg gct gcc tcc ttc aac tgc atc 1590
389 Leu Ala Val Leu Gly Lys Gly Cys Leu Ala Ala Ser Phe Asn Cys Ile 440
390 430 435
392 ttc ctg tat act ggg gaa ctg tat ccc aca atg atc cgg cag aca ggc 1638
393 Phe Leu Tyr Thr Gly Glu Leu Tyr Pro Thr Met Ile Arg Gln Thr Gly 455
394 445 450
396 atg gga atg ggc agc acc atg gcc cga gtg ggc agc atc gtg agc cca 1686
397 Met Gly Met Gly Ser Thr Met Ala Arg Val Gly Ser Ile Val Ser Pro 470
398 460 465
400 ctg gtg agc atg act gcc gag ctc tac ccc tcc atg cct ctc ttc atc 1734
401 Leu Val Ser Met Thr Ala Glu Leu Tyr Pro Ser Met Pro Leu Phe Ile 485
402 475 480
404 tac ggt gct gtt cct gtg gcc gcc agc gct gtc act gtc ctc ctg cca 1782
405 Tyr Gly Ala Val Pro Val Ala Ala Ser Ala Val Thr Val Leu Leu Pro 505
406 490 495 500
408 gag acc ctg ggc cag cca ctg cca gac acg gtg cag gac ctg gag agc 1830
409 Glu Thr Leu Gly Gln Pro Leu Pro Asp Thr Val Gln Asp Leu Glu Ser 520
410 510 515
412 agg tgg gcc ccc act cag aaa gaa gca ggg ata tat ccc agg aaa ggg 1878
413 Arg Trp Ala Pro Thr Gln Lys Glu Ala Gly Ile Tyr Pro Arg Lys Gly 535
414 525 530
416 aaa cag acg cga cag caa caa gag cac cag aag tat atg gtc cca ctg 1926
417 Lys Gln Thr Arg Gln Gln Gln Glu His Gln Lys Tyr Met Val Pro Leu 550
418 540 545
420 cag gcc tca gca caa gag aag aat gga ctc tgaggactga gaaggggcct 1976
421 Gln Ala Ser Ala Gln Glu Lys Asn Gly Leu 560
422 555
424 tacagaaccc taaagggagg gaaggtccta caggtctccg gccacccaca caaggaggag 2036
425 gaagaggaaa tgggtgaccca agtgtggggg ttgtggttca ggaaagcatc ttcccagggg 2096
426 tccacctccc tttataaacc ccaccagaac cacatcatta aaaggtttga ctgcgaaaaa 2156
E--> 427 aaaaaaaaaa aaaaa 2171

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/424,347

DATE: 04/30/2002

TIME: 14:45:50

Input Set : A:\49429seq.txt

Output Set: N:\CRF3\04302002\I424347.raw

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:273 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:3, CDS LOCATION: (268)...
(1956)
L:427 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:2171 SEQ:3